

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/918,874DATE: 04/10/98
TIME: 14:40:15

INPUT SET: S24895.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ashkenazi et al.
6
7 (ii) TITLE OF INVENTION: RTD Receptor
8
9 (iii) NUMBER OF SEQUENCES: 5
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Genentech, Inc.
13 (B) STREET: 1 DNA Way
14 (C) CITY: South San Francisco
15 (D) STATE: California
16 (E) COUNTRY: USA
17 (F) ZIP: 94080
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: WinPatin (Genentech)
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER:
27 (B) FILING DATE:
28 (C) CLASSIFICATION:
29
30 (viii) ATTORNEY/AGENT INFORMATION:
31 (A) NAME: Marschang, Diane L.
32 (B) REGISTRATION NUMBER: 35,600
33 (C) REFERENCE/DOCKET NUMBER: P1129
34
35 (ix) TELECOMMUNICATION INFORMATION:
36 (A) TELEPHONE: 650/225-5416
37 (B) TELEFAX: 650/952-9881
38 (2) INFORMATION FOR SEQ ID NO:1:
39
40 (i) SEQUENCE CHARACTERISTICS:
41 (A) LENGTH: 386 amino acids
42 (B) TYPE: Amino Acid
43 (D) TOPOLOGY: Linear
44
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
46

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47	Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg	
48	1 5 10 15	
49		
50	Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro	
51	20 25 30	
52		
53	Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val	
54	35 40 45	
55		
56	Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg	
57	50 55 60	
58		
59	Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg	
60	65 70 75	
61		
62	Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser	
63	80 85 90	
64		
65	Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr	
66	95 100 105	
67		
68	Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val	
69	110 115 120	
70		
71	Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg	
72	125 130 135	
73		
74	Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn	
75	140 145 150	
76		
77	Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly	
78	155 160 165	
79		
80	Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys	
81	170 175 180	
82		
83	Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala	
84	185 190 195	
85		
86	Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr	
87	200 205 210	
88		
89	His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val	
90	215 220 225	
91		
92	Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu	
93	230 235 240	
94		
95	Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His	
96	245 250 255	
97		
98	Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly	
99	260 265 270	

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100
101   Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
102                               275                      280                      285
103
104   Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
105                               290                      295                      300
106
107   Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
108                               305                      310                      315
109
110   Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
111                               320                      325                      330
112
113   Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
114                               335                      340                      345
115
116   Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
117                               350                      355                      360
118
119   Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
120                               365                      370                      375
121
122   Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
123                               380                      385 386
124

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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135
136   CCAACTGCAC CTCGGTTCTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG 50
137
138   ATCCCTCGAC CTCGACCCAC GCGTCCGGAA CCTTTGCACG CGCACAAACT 100
139
140   ACGGGGACGA TTTCTGATTG ATTTTGGCG CTTTCGATCC ACCCTCCTCC 150
141
142   CTTCTC  ATG GGA CTT TGG GGA CAA AGC GTC CCG ACC GCC 189
143           Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
144           1             5             10
145
146   TCG AGC GCT CGA GCA GGG CGC TAT CCA GGA GCC AGG ACA 228
147   Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
148           15             20
149
150   GCG TCG GGA ACC AGA CCA TGG CTC CTG GAC CCC AAG ATC 267
151   Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
152           25             30             35

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153															
154	CTT	AAG	TTC	GTC	GTC	TTC	ATC	GTC	GCG	GTT	CTG	CTG	CCG	306	
155	Leu	Lys	Phe	Val	Val	Phe	Ile	Val	Ala	Val	Leu	Leu	Pro		
156			40					45					50		
157															
158	GTC	CGG	GTT	GAC	TCT	GCC	ACC	ATC	CCC	CGG	CAG	GAC	GAA	345	
159	Val	Arg	Val	Asp	Ser	Ala	Thr	Ile	Pro	Arg	Gln	Asp	Glu		
160					55					60					
161															
162	GTT	CCC	CAG	CAG	ACA	GTG	GCC	CCA	CAG	CAA	CAG	AGG	CGC	384	
163	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg	Arg		
164		65					70					75			
165															
166	AGC	CTC	AAG	GAG	GAG	GAG	TGT	CCA	GCA	GGA	TCT	CAT	AGA	423	
167	Ser	Leu	Lys	Glu	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg		
168				80					85						
169															
170	TCA	GAA	TAT	ACT	GGA	GCC	TGT	AAC	CCG	TGC	ACA	GAG	GGT	462	
171	Ser	Glu	Tyr	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly		
172	90					95					100				
173															
174	GTG	GAT	TAC	ACC	ATT	GCT	TCC	AAC	AAT	TTG	CCT	TCT	TGC	501	
175	Val	Asp	Tyr	Thr	Ile	Ala	Ser	Asn	Asn	Leu	Pro	Ser	Cys		
176			105					110					115		
177															
178	CTG	CTA	TGT	ACA	GTT	TGT	AAA	TCA	GGT	CAA	ACA	AAT	AAA	540	
179	Leu	Leu	Cys	Thr	Val	Cys	Lys	Ser	Gly	Gln	Thr	Asn	Lys		
180					120					125					
181															
182	AGT	TCC	TGT	ACC	ACG	ACC	AGA	GAC	ACC	GTG	TGT	CAG	TGT	579	
183	Ser	Ser	Cys	Thr	Thr	Thr	Arg	Asp	Thr	Val	Cys	Gln	Cys		
184		130					135					140			
185															
186	GAA	AAA	GGA	AGC	TTC	CAG	GAT	AAA	AAC	TCC	CCT	GAG	ATG	618	
187	Glu	Lys	Gly	Ser	Phe	Gln	Asp	Lys	Asn	Ser	Pro	Glu	Met		
188				145					150						
189															
190	TGC	CGG	ACG	TGT	AGA	ACA	GGG	TGT	CCC	AGA	GGG	ATG	GTC	657	
191	Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val		
192	155					160					165				
193															
194	AAG	GTC	AGT	AAT	TGT	ACG	CCC	CGG	AGT	GAC	ATC	AAG	TGC	696	
195	Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys		
196			170					175					180		
197															
198	AAA	AAT	GAA	TCA	GCT	GCC	AGT	TCC	ACT	GGG	AAA	ACC	CCA	735	
199	Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro		

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206   GCC TCT CCC TAT CAC TAC CTT ATC ATC ATA GTG GTT TTA 813
207   Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu
208           210           215
209
210   GTC ATC ATT TTA GCT GTG GTT GTG GTT GGC TTT TCA TGT 852
211   Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys
212   220           225           230
213
214   CGG AAG AAA TTC ATT TCT TAC CTC AAA GGC ATC TGC TCA 891
215   Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser
216           235           240           245
217
218   GGT GGT GGA GGA GGT CCC GAA CGT GTG CAC AGA GTC CTT 930
219   Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu
220           250           255
221
222   TTC CGG CGG CGT TCA TGT CCT TCA CGA GTT CCT GGG GCG 969
223   Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
224           260           265           270
225
226   GAG GAC AAT GCC CGC AAC GAG ACC CTG AGT AAC AGA TAC 1008
227   Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
228           275           280
229
230   TTG CAG CCC ACC CAG GTC TCT GAG CAG GAA ATC CAA GGT 1047
231   Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
232   285           290           295
233
234   CAG GAG CTG GCA GAG CTA ACA GGT GTG ACT GTA GAG TYG 1086
235   Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
236           300           305           310
237
238   CCA GAG GAG CCA CAG CGT CTG CTG GAA CAG GCA GAA GCT 1125
239   Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
240           315           320
241
242   GAA GGG TGT CAG AGG AGG AGG CTG CTG GTT CCA GTG AAT 1164
243   Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
244           325           330           335
245
246   GAC GCT GAC TCC GCT GAC ATC AGC ACC TTG CTG GAT GCC 1203
247   Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
248           340           345
249
250   TCG GCA ACA CTG GAA GAA GGA CAT GCA AAG GAA ACA ATT 1242
251   Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
252   350           355           360
253
254   CAG GAC CAA CTG GTG GGC TCC GAA AAG CTC TTT TAT GAA 1281
255   Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
256           365           370           375
257
258   GAA GAT GAG GCA GGC TCT GCT ACG TCC TGC CTG TGAAAG 1320

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text